

FIG. 1

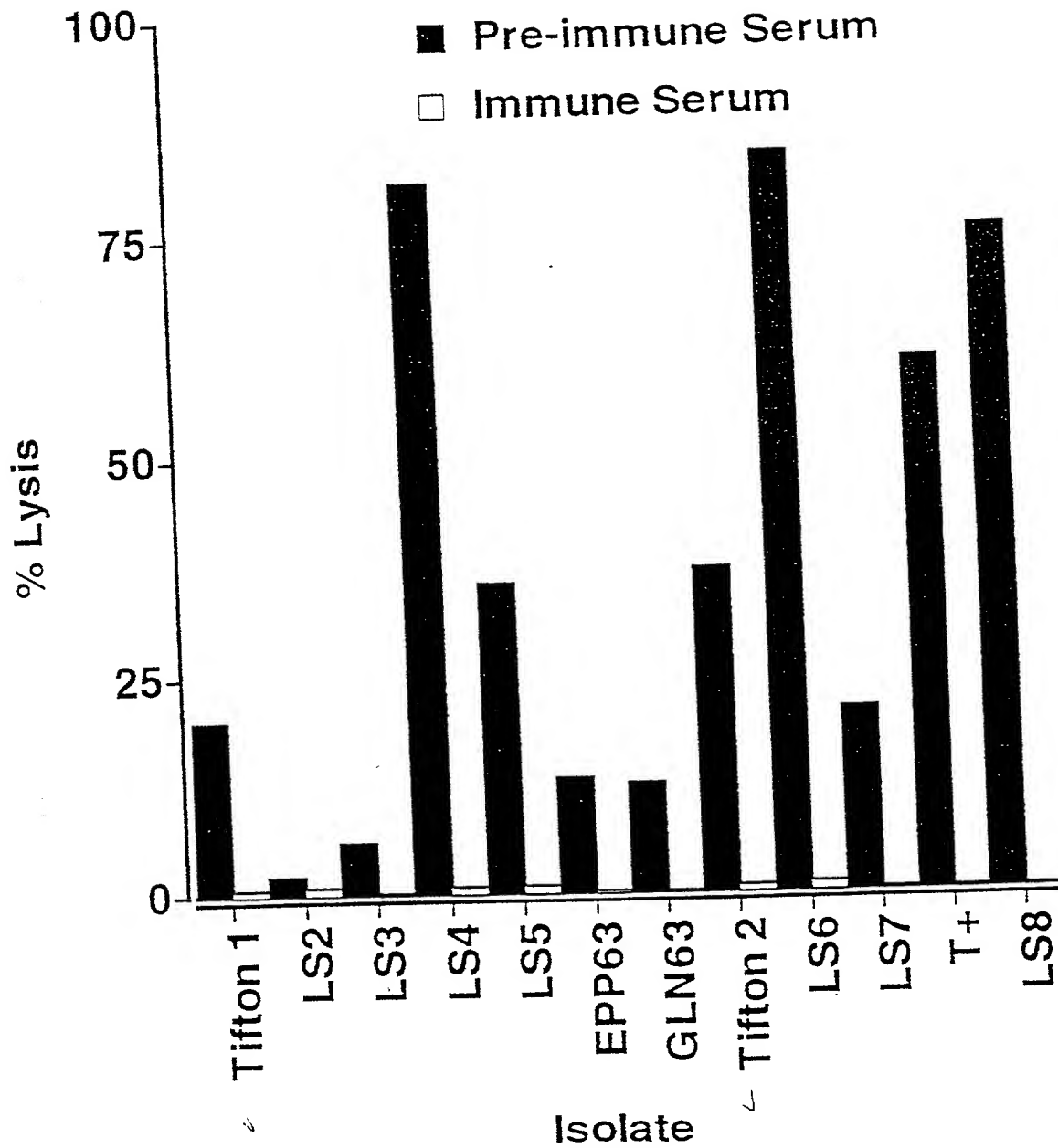
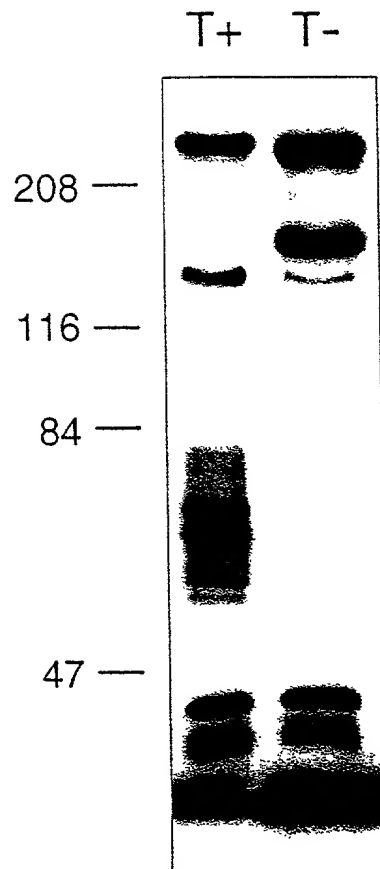


FIG. 2



Appendix A update-July 1999

Bases 1-1200

Amino acids 1-400

1	ATGTCCAATATAAATGTAATTAATCTAATATTCAAGCAGGCTTGAATTCAACAAAGTCT	60
1	M S N I N V I K S N I Q A G L N S T K S	20
61	GGATTAATAAATCTTTACTTGGCTATTCCTAAAGATTATGATCCGCAAAAAGGTGGGACT	120
21	G L K N L Y L A I P K D Y D P Q K G G T	40
121	TTAAATGATTTTATTAAGCTGCTGATGAATTAGGTATTGCTCGTTTAGCAGAAGAGCCT	180
41	L N D F I K A A D E L G I A R L A E E P	60
181	AATCACACTGAAACAGCAAAAAATCTGTTGACACAGTAAATCAGTTTCTCTCTCACA	240
61	N H T E T A K K S V D T V N Q F L S L T	80
241	CAAACTGGTATTGCTATTTCTGCAACAAAATTAGAAAAGTTCTTACAAAAACATTCTACC	300
81	Q T G I A I S A T K L E K F L Q K H S T	100
301	AATAAGTTAGCCAAAGGGTTAGACAGTGTAGAAAATATTGATCGTAAATTAGGTAAAGCA	360
101	N K L A K G L D S V E N I D R K L G K A	120
361	AGTAATGTATTATCAACATTAAGCTCTTTTTGGGCACTGCATTAGCGGGTATAGAACTT	420
121	S N V L S T L S S F L G T A L A G I E L	140
421	GATTCTTTAATCAAAAAAGGTGATGCTGCACCTGATGCTTTGGCTAAAGCTAGTATTGAC	480
141	D S L I K K G D A A P D A L A K A S I D	160
481	TTGATTAATGAGATAATTGGTAATCTATCTCAGAGTACTCAAACGATTGAAGCATTTTCT	540
161	L I N E I I G N L S Q S T Q T I E A F S	180
541	TCACAGTTAGCAAAGTTAGGTTCTACTATATCGCAGGCTAAAGGCTTCTCTAATATAGGA	600
181	S Q L A K L G S T I S Q A K G F S N I G	200
601	AACAAGTTGCAAACTTAAATTTTTCTAAACAAATCTTGGTTTGGAAATAATTACTGGT	660
201	N K L Q N L N F S K T N L G L E I I T G	220
661	TTGCTATCAGGCATTTCTGCAGGCTTTGCTTTAGCGGATAAAAAATGCATCGACTGGCAAA	720
221	L L S G I S A G F A L A D K N A S T G K	240
721	AAAGTTGCTGCAGGTTTTGAATTAAGCAATCAAGTTATTGGTAATGTAACAAAGCAATT	780
241	K V A A G F E L S N Q V I G N V T K A I	260
781	TCTTCATATGTTTTAGCACAACTGTTGCTGCTGGTCTATCACTACTGGTGCTGTTGCT	840
261	S S Y V L A Q R V A A G L S T T G A V A	280
841	GCTTTAATTACTTCATCGATTATGTTGGCAATTAGTCCTTTGGCATTATGAATGCAGCA	900
281	A L I T S S I M L A I S P L A F M N A A	300
901	GATAAATTCAATCATGCTAATGCTCTTGATGAGTTTGCAAAACAATCCGAAAATTTGGC	960
301	D K F N H A N A L D E F A K Q F R K F G	320
961	TATGATGGGGATCATTTATTGGCTGAATATCAGCGTGGTGTGGGTACTATTGAAGCTTCA	1020
321	Y D G D H L L A E Y Q R G V G T I E A S	340
1021	TTAACTACAATTAGTACGGCATTAGGTGCAGTTTCTGCTGGTGTTCGCTGCTGCTGTA	1080
341	L T T I S T A L G A V S A G V S A A A V	360
1081	GGATCTGCTGTTGGTGCACCGATTGCACTATTAGTTGCAGGTGTTACAGGATTGATCTCT	1140
361	G S A V G A P I A L L V A G V T G L I S	380
1141	GGAATTTTAGAAGCGTCTAAACAGGCAATGTTTGAAAGTGTGCTAACCGTTTACAAGGT	1200
381	G I L E A S K Q A M F E S V A N R L Q G	400

moxA
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MoxA

Appendix A update-July 1999, continued

Bases 1201-2400

Amino acids 401-800

1201	AAAATTTTAGAGTGGGAAAAGCAAATGGCGGTCAGAACTATTTTGATAAAGGCTATGAT	1260
401	K I L E W E K Q N G G Q N Y F D K G Y D	420
1261	TCTCGTTATGCTGCTTATTTAGCTAATAACTTAAATTTTTGTCTGAGCTAAATAAGAG	1320
421	S R Y A A Y L A N N L K F L S E L N K E	440
1321	TTGGAAGCTGAACGTGTTATTGCAATCACCCAACAACGTTGGGATAATAATATTGGTGAG	1380
441	L E A E R V I A I T Q Q R W D N N I G E	460
1381	TTAGCAGGTATTACCAAATTGGGTGAACGCATTAAGAGCGGAAAAGCTTATGCAGATGCT	1440
461	L A G I T K L G E R I K S G K A Y A D A	480
1441	TTTGAAGATGGCAAGAAAGTTGAAGCTGGTTCCAATATTACTTTGGATGCTAAACTGGT	1500
481	F E D G K K V E A G S N I T L D A K T G	500
1501	ATCATAGACATTAGTAATTCAAATGGGAAAAAACGCAAGCGTTGCATTTCACTTCGCCT	1560
501	I I D I S N S N G K K T Q A L H F T S P	520
1561	TTGTTAACAGCAGGAAGTGAATCACGTGAACGTTTAACTAATGGTAAATACTCTTATATT	1620
521	L L T A G T E S R E R L T N G K Y S Y I	540
1621	AATAAGTTAAAATTCGGACGTGTAATAACTGGCAAGTTACAGATGGAGAGGCTAGTTCT	1680
541	N K L K F G R V K N W Q V T D G E A S S	560
1681	AAATTAGATTTCTCTAAAGTTATTCAGCGTGTAGCCGAGACAGAAGGCACAGACGAGATT	1740
561	K L D F S K V I Q R V A E T E G T D E I	580
1741	GGTCTAATAGTAAATGCAAAAGCTGGCAATGACGATATCTTTGTTGGTCAAGGTAAAATG	1800
581	G L I V N A K A G N D D I F V G Q G K M	600
1801	AATATTGATGGTGGAGATGGACACGATCGTGTCTTCTATAGTAAAGACGGAGGATTTGGT	1860
601	N I D G G D G H D R V F Y S K D G G F G	620
1861	AATATTACTGTAGATGGTACGAGTGCAACAGAAGCAGGCAGTTATACAGTTAATCGTAAG	1920
621	N I T V D G T S A T E A G S Y T V N R K	640
1921	GTTGCTCGAGGTGATATCTACCATGAAGTTGTGAAGCGTCAAGAAACCAAGGTGGGTAAA	1980
641	V A R G D I Y H E V V K R Q E T K V G K	660
1981	CGTACTGAAACTATCCAGTATCGTGATTATGAATTAAGAAAAGTTGGGTATGGTTATCAG	2040
661	R T E T I Q Y R D Y E L R K V G Y G Y Q	680
2041	TCTACCGATAATTTGAAATCAGTAGAAGAAGTAATTGGTTCTCAATTTAATGATGTATTC	2100
681	S T D N L K S V E E V I G S Q F N D V F	700
2101	AAAGGTTCTAAATTCAACGACATATTCATAGTGGTGAAGGTGATGATTTACTCGATGGT	2160
701	K G S K F N D I F H S G E G D D L L D G	720
2161	GGTGCTGGTGACGACCGCTTGTGTTGGTGGTAAAGGCAACGATCGACTTTCTGGAGATGAA	2220
721	G A G D D R L F G G K G N D R L S G D E	740
2221	GGCGATGATTTACTCGATGGCGGTTCTGGTGATGATGATTAATGGTGGTGCTGGTAAT	2280
741	G D D L L D G G S G D D V L N G G A G N	760
2281	GATGTCTATATCTTTGCGAAAGGTGATGGTAATGATACTTTGTACGATGGCACGGGCAAT	2340
761	D V Y I F R K G D G N D T L Y D G T G N	780
2341	GATAAATTAGCATTTGCAGATGCAAAATATCTGATATTATGATTGAACGTACCAAAGAG	2400
781	D K L A F A D A N I S D I M I E R T K E	800

1201-2400 bases

Appendix A update-July 1999, continued

Bases 2401-2784

Amino acids 801-927

2401	GGTATTATAGTTAAACGAAATGATCATTGAGGTAGTATTAACATACCAAGATGGTACATA	2460
801	G I I V K R N D H S G S I N I P R W Y I	820
2461	ACATCAAATTTACAAAATTATCAAAGTAATAAAACAGATCATAAAATTGAGCAACTAATT	2520
821	T S N L Q N Y Q S N K T D H K I E Q L I	840
2521	GGTAAAGATGGTAGTTATATCACTTCCGATCAAATTGATAAAATTTTGCAAGATAAGAAA	2580
841	G K D G S Y I T S D Q I D K I L Q D K K	860
2581	GATGGTACAGTAATTACATCTCAAGAATTGAAAAAGCTTGCTGATGAGAATAAGAGCCAA	2640
861	D G T V I T S Q E L K K L A D E N K S Q	880
2641	AAATTATCTGCTTCGGACATTGCAAGTAGCTTAAATAAGCTAGTTGGGTCAATGGCACTA	2700
881	K L S A S D I A S S L N K L V G S M A L	900
2701	TTTGGTACAGCAAATAGTGTGAGTTCTAACGCCTTACAGCCAATTACACAACCAACTCAA	2760
901	F G T A N S V S S N A L Q P I T Q P T Q	920
2761	GGAATTTTGGCTCCAAGTGTTTAG	2784
921	G I L A P S V *	928

SEQ ID NO: 1
SEQ ID NO: 2

[illegible]

MbxA	- - - - - A R T T T S	N G C T T T T A T	K S G D T M S N I N	V K K S N I O A G L	N C S S G L R N L	Y H A F K K Q V	D P Q K G	38
LkA	M S K T L L S S L K	S G Q Q G L K N G	A N N L S A G T T	L N G L L D G G C	H L A L O N G A R L	I L L T P Q G	D T E O G	39
ApXIIA	M P T T L T A A Q L K	S L A Q S A K Q S A	A N N L S A G T T	L N G L L D G G C	Q T R N A G . N _ L	I L L T P Q G	D S G O G	62
HlyA								61
MbxA	G T L N D L V K A A	D L G L G A R L A E	E P N H K T A T A K	S V D T V N Q F L S	L T T G I A I S A	T K L F F L Q H	S N H L	103
LkA	N G V Q D L V K A A	N L G L G A R L A E	E N S L L T A T A K	S L G D T T O M T L G	L T E N G I V I S A	P O L D X L L O X	N P H I	121
ApXIIA	S S N Q D L V _ T A	D E G L E V Q Y	L N G L L T T M Q	V L G A _ K L T L G	L T E N G I V I F A	P O L D X L L O X	Q . . K A	125
HlyA								124
MbxA	A K G L . D S V E N	F D R K L G K A S N	V L S T _ S S F L G	T A L A G I E L D S	M I K K G D	A A P D A L A K A S	I L I N	163
LkA	Q Q A L . G S A S S	H V G N A N K A K T	V L S G T F G S I L G	S V L S A G M V L D E	A L Q N N	S N Q H A R L A K A G	L E L T W	180
ApXIIA	G N K L G G S A N	H G D N L G K A G S	V L S T F G N F L G	T A L S S N K L D E	M I K K Q K S G G N	V S S S E L A K A G	T E L I N	185
HlyA								189
MbxA	L T G N S Q S T	O R T A P S S O L	A K L G S K T _ S O A	K G L F S N _ G N K L	Q M L M F S K T N	L G L I I N G L L	S G I S A	227
LkA	S T E I E I A N S Q	K L N D E G S O I	S Q F G S K T _ S O I	K G L F S N T L G O R L	N _ G G L D K A G	L G L D I S G L L	S G A T A	245
ApXIIA	S L V G S I A S S	Q T V D A F A S Q I	K L G S H I S M V	K L G L G V S N K L	Q M L M F L G R A S	L G L D I S G L L	S G A S A	250
HlyA	L V . D T A A S L	N N N S _ S _ O L	N K L G S V L S M T	K H L N G L V G R K L	O R I P N L D N I G	A G L D T _ S G L	S A I S A	253
MbxA	G F A L A D R N A S	H G K K V A G C F F	L S N O V I C H V	K A I S S Y L L A O	R V A A C L S T T C	A V A A L I S S _	M L A I S	292
LkA	A L _ L A D R N A S	H G K K V A G C F F	F A R A T C S V	K A V S S Y L L A O	R V A A C L S T T C	P U A A L I A S V	S L A I S	310
ApXIIA	S F L L S N A D A D	T G N K A A A G V E	L T T K V _ O R V G	R G I S Q T I _ A O	R V A A C L S T T C	P U A A L I A S V	A L A _	315
HlyA								318
MbxA	L A F _ N A R D R	F N H A L _ S _	A K O F R F G Y D	G D H L L A E Y Q R	G V G T I A S L T	F I S T A L G A V S	A G V S A	357
LkA	P L A F A G L A D R	F N K Q L S L S V	A E R F F R L C G D	G D N R L L A E Y Q R	G R G R T D A S V	A I N T A L A A	C G V S A	375
ApXIIA	T E S L S L A D R	K K R A K I E	S _ R F R K L C D	G B S L L A A F H	E C A K D A S L	R I S T V L A S V	S G _ S A	380
HlyA								383
MbxA	A A V G S A V G A P	I A L L V A G V T G	L I S G I L R A S N	Q A M F E S V A N	L Q K I L E W E N	Q N G G Q N I F K	G I D S R	422
LkA	A A A G S V _ A S P	I A L L V S _ T G	V I S T I L Y S K	Q A M F E S V A N K	I N N K I V E W E N	P V N G G N I F F N	G I D A R	440
ApXIIA	A A T S L V G A P	V A L L V A G V T G	L I T T I L E Y S K	Q A M F E S V A N K	V M D I V E W E N	. K N G K N I F F N	G I D S R	447
HlyA	A A T S L V G A P	V S A L L V A G V T G	_ I S G I L R A S N	Q A M F E S V A N K	A D V I L E W E N	. K N G K N I F F N	G I D A R	447
peak 23								
MbxA	Y A A Y L A N N _ K	F L S L A S S L	A E R V I A I T O Q	R W D N N I G S L A	G I T _ L G R _ T K	S G K A Y A D A P E	_ G N K V	487
LkA	Y L A N L O D N M K	F L N L S L K L O	A E R V I A I T O Q	Q W D N N I G D L A	G I S R L C K _ K	S G K A Y V D A P E	G G K _	505
ApXIIA	H L A D L O D N M K	F L I N L S L K L O	A E R V I A I T O Q	R W D N N I G D L A	A I S R L C K _ K	S G K A Y V D A P E	E C Q H Q	509
HlyA	H A A F L D N F K	I L S Q Y K E Y S	V E R S V L I T O Q	R W D T L I G E L A	G _ T R N G N T L	S G K S Y _ D Y _	E C R L	512
MbxA	E A G S L V	T L D A K _ C I D	I S N S N G K K T O	A H E F T S P L L T	A G T E S R E R L T	N G K Y S Y I N K L	K F G R V	548
LkA	K L _ _ _ . S S V	T L D S A N G I D	I S S G K A K T O	H L E R T S P L L T	P G T E S R E R L T	T G K Y S Y I N K L	N _ N R V	566
ApXIIA	S T D _ _ . S S V	O L D N K N C I T	I S H T M R _ K T O	S V L E R T S P L L T	P G E S _ R E R L T	E G K N S Y I T E L	H L K V	569
HlyA	K K X P D E F Q K Q	V F D P L K G N E D	L S D S _ . K S S T	L K E F V T S P L L T	P G E S _ R E R L T	S G K Y S Y I T E L	L L K G V	575
MbxA	K N _ Q V T D . G	A S S K L D F S K V	I Q R A _ E L D N	S G _ T D E I T	G _ I V N A K A G N	D D V F V G S G T T	H D G G	605
LkA	D S K _ T D . G A	A S S K L D F S K V	V O R I G A _ E L D N	A G N V T K K E I T	K I I A K L A G N	D D V F V G S G T T	H D G G	630
ApXIIA	D E S T V T D . G	A S S K L D F S K V	V O R I G A _ E L D N	A G N I T E S K T	K I I A K L A G N	D D V F V G S G T T	H D G G	633
HlyA	D K X P D E F Q K Q	K G S V Y D _ S E	I O H A S V _	T G E _ N Q Y _ E I	H E S H L G D G D	D K V F L S A G S A	N H Y A G	634
MbxA	D G H R V F Y S K	D G G _ G N T _ D	G T S A T E A G S Y	T V M R K V . A R G	D I Y H E V K R Q	E T X V G K R T E T	T O T A D	669
LkA	G C D R V H Y S R	. G N Y G A L C I D	A T K K T E Q G S Y	T V N R F V . E T G	K A L R E V T S T H	T A L V G K N R E E T	T O T A D	692
ApXIIA	D C D R V H Y S R	. G N Y G A L C I D	A T A T E T E K G S Y	S V K R Y V . G D S	K A L R E V T S T H	T A L V G K N R E E T	T O T A D	695
HlyA	K C H R V F Y S K	T . D T G Y L T D	G T N A T E A G N Y	G T N V L G C D V	K V L Q E V R V R Q	E V S V G K R T E T	T O T A D	698
peak 26								
MbxA	Y L L R K V . G Y G	Y Q S T D N L K S V	E E I I G T S O F N D	F K G S K F N D I	F H S G G D D L T	D G A G D D D R L F	G G K G D	733
LkA	S N Q H . R A G	Y T T K D N L K A V	E E I I G T S O F N D	F K G S K F N D A	F N S G G G V D D T	D G N D G D D R L F	G G K G D	756
ApXIIA	R D D F R . H T C	Y T V T D S L K S V	E E I I G T S O F N D	F K G S Q F D D I	F N G A G G V D D T	D G N D G D D R L F	G G K G D	759
HlyA	Y F T T H I N G K N	L T E T D N L Y S V	E E I I G T T R A D	K F G S K F N D I	F N G A G D D D H I	L G N D G N D D R L F	G G K G D	763
MbxA	D R _ S G G E G D	742
LkA	D R _ S G G E G D	765
ApXIIA	D R _ S G G E G D	768
HlyA	D R _ S G G E G D .	Q L Y G G D G N D K	L I G G A G N N Y L	N G G O G D D E L Q	V Q G N S L A K N V	L S G G K G N D K L	Y G S E G	828
MbxA	D L L D G G S G D	D V L N G G A G N D	Y F R K G D G N	D T Y D G T G . N	D K L A F A D A N N	S D M I E R T H E	G T Y K	805
LkA	D L L D G G S G D	D L L N G G A G N D	Y F R K G D G N	D T Y D G T G . N	D K L A F A D A N N	S D M I E R T H E	G T Y K	827
ApXIIA	D L L D G G S G D	D L L N G G A G N D	Y F R K G D G N	D T Y D G T G . N	D K L A F A D A N N	S D M I E R T H E	G T Y K	830
HlyA	A D L L D G G S G N	D L L K G G Y G N D	L L G L S G Y G H	H L D D D G G K O	D R L S L A D I T F	L V A L A R R E G N	D C L M Y	893
MbxA	R N D	H S G S I N I P R W	T _ _ _ _ I T S N L	Q N Y Q S N M T D R	K I E Q _ I G K D G	S Y I T S D Q F D D	L L Q D K	859
LkA	T N S	K G E R V I R I C N W	K E A D F L A K E V	P N X K A T N . D R	E R I T S I G K D G	E R I T S Q V D D	L L _ A	882
ApXIIA	K A S G N V L S I G	K G E R V I R I C N W	K E K E _ S G D V	S K _ Q _	K I E Q _ I G K D G	E R I T S Q V D D	L L _ A	885
HlyA		H N G I G I F I C N W			K I E Q _ I G K D G	E R I T S Q V D D	A L E Y Q	949
MbxA	K D G T V T S Q E	L K R L A D E N K S	Q L S A S D _ A S	S L N K M _ S M A	L F G T A N S V S S	N A L Q P I T Q P T	Q G I L A	924
LkA	K G N G K I N Q D E	L S K V V D N D Y L	L K _ H S K N V T S	S L D K L S S V S	A F _ T S S S N D S R	N V L _ V A . F T	_ S M L D	945
ApXIIA	E G N G K I N Q D E	L S K V V D N D Y L	S M _ D R Q N V S W	S L A K L I S S V S	S F _ T S S S D F N	N V L _ V A . F T	_ S M L D	945
HlyA	Q S N N K _ A S Y V	Y G N D A L A Y G S	_ Q G N L N P L I N	E S _ K R I S A A G	N M D V K E E R A A	A S _ L Q L S G . N	A S D F S	1011
MbxA	P S G L S _ _ _ _	--	927					
LkA	Q S L S _ _ _ _	--	953					
ApXIIA	V S _ _ _ _	--	956					
HlyA	Y G R N S I T L F A	S A	1023					

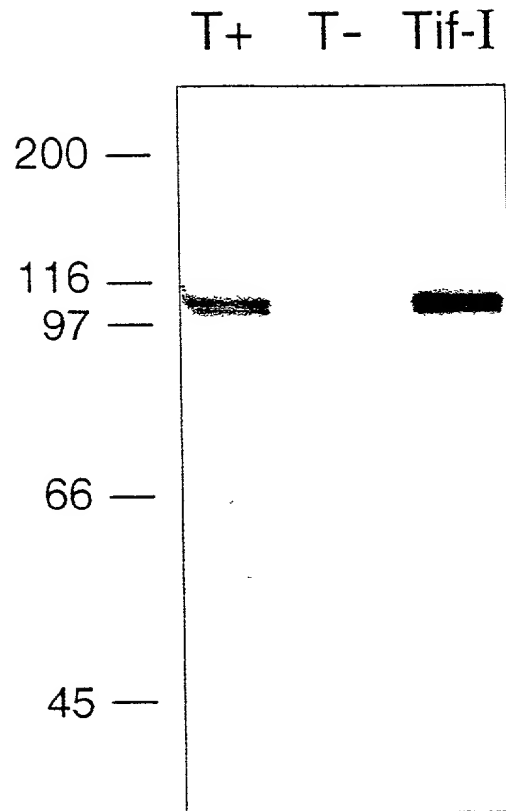
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FIG. 6

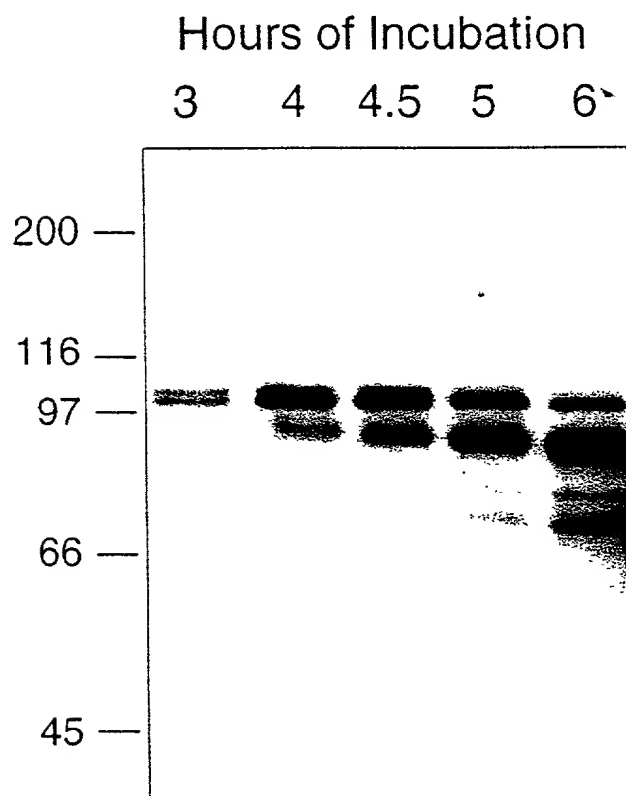
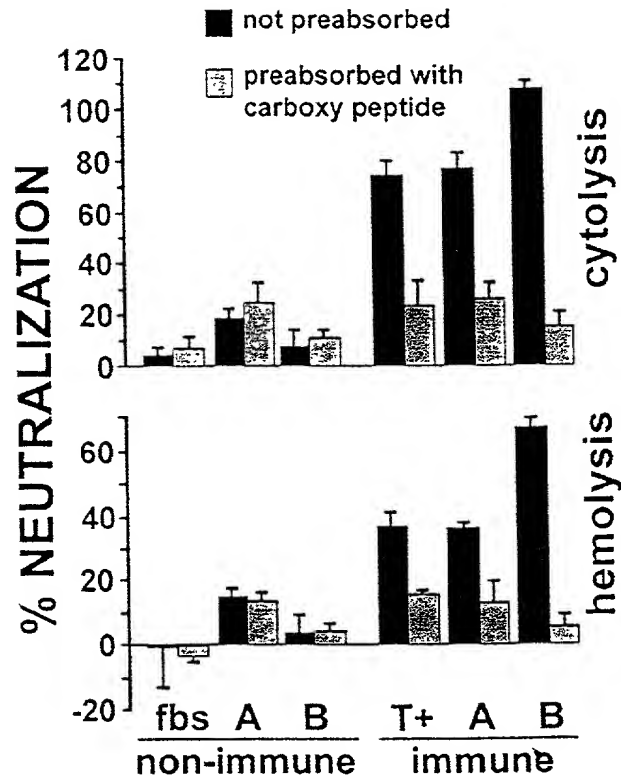


FIG. 7



1 ATGGGTGGTGATACTTCTTTAATTAGACTTAATTTACAAACCTTAATAGTAATTTAGTT 60
 1 M G G D T S L I R L N L Q T L N S N L V 20
 61 ATGATAGATTATGCTCAACAACCTGCTCTATCTGCTCTGTTATCCTTGCCAAATACTAT 120
 21 M I D Y A Q Q P A L S A L V I L A K Y Y 40
 121 GGTATTTCTGCAAGTCCAGCAGACATTATGCATCAGTTTTCTGATAATACAAAAGGAGAC 180
 41 G I S A S P A D I M H Q F S D N T K G D 60
 181 CTGAATGAAATTGAATGGATGTTGGCAGCAAAGAAATTAGAATTAAAGGTAAAGATTATA 240
 61 L N E I E W M L A A K K L E L K V K I I 80
 241 AAACAGCCTTTAACTCGATTGTCAATGATAACACTTCCTGCTTTGGTGTGGTGTGATAAT 300
 81 K Q P L T R L S M I T L P A L V W C D N 100
 301 AAGCCCGATTAGATCAAAATTTAACTCTCATTTTATACTAACTAAAATTGATGGGGTG 360
 101 K P D L D Q N L N S H F I L T K I D G V 120
 361 GGATCTGCTGCAAAATATCTCATCTACGATTTGATTGAGAATCGTCCATAATATTAGAT 420
 121 G S A A K Y L I Y D L I E N R P I I L D 140
 421 GCAAGTGAGTTTTCTGAAAGATATTCTGGTAAGTTAATGCTAGTAACTTCCCGTGGTCA 480
 141 A S E F S E R Y S G K L M L V T S R A S 160
 481 ATATTGGGTTCAATTGGCTAAATTTGATTTTACTTGGTTTATTCCTGCGTAATCAAATAT 540
 161 I L G S L A K F D F T W F I P A V I K Y 180
 541 CGTTATATTTTTTTGAAGTCATCGTTATTTTCACTGGTGTACAGATTTTTGCTCTGATT 600
 181 R Y I F F E V I V I S V V L Q I F A L I 200
 601 ACGCCATTGTTTTTTCAGGTTGTGATGGATAAGGTATTGGTGCATCGTGGTTTTTCTACT 660
 201 T P L F F Q V V M D K V L V H R G F S T 220
 661 CTGGATGTGGTAGCGATTGCCTTGTGGTAGTAAGTTTATTTGAAGTCATTTTAAGTGGT 720
 221 L D V V A I A L L V V S L F E V I L S G 240
 721 CTACGCACTTATATTTTTGCTCATACAACCTCTCGAATTGATGTAGAGCTAGGAGCACGA 780
 241 L R T Y I F A H T T S R I D V E L G A R 260
 781 TTATTTTCGTCATCTATTAGCTCTACCGCTTGCTTATTTTGAAGTAGAAGAGTAGGCGAT 840
 261 L F R H L L A L P L A Y F E S R R V G D 280
 841 ACAGTTGCACGTATACGTGAATTGGAACATATCCGCAATTTCTTAACTGGTCAAGCTCTC 900
 281 T V A R I R E L E H I R N F L T G Q A L 300
 901 ACTTCAGTTTTAGATTTGGTGTCTTTTATATTCTTGTGTGAATGTGGTATTACAGC 960
 301 T S V L D L V F S F I F L F V M W Y Y S 320
 961 CCTACTTTAACTGGTAGTTTTGGCATCATTACCAATATATGCGTTTTGGTCTGCCTTT 1020
 321 P T L T L V V L A S L P I Y A F W S A F 340
 1021 ATTAGCCCAATTTTACGCACTCGACTAAATGATCAATTTGCACGCAATGCAGATAATCAA 1080
 341 I S P I L R T R L N D Q F A R N A D N Q 360
 1081 TCTTTTTTAGTGGAAAGTATTACTGCGGTTGGTACGGTAAAAGCAATGGCAGTTGAACCT 1140
 361 S F L V E S I T A V G T V K A M A V E P 380
 1141 CAAATGACCCGCTCGCTGGGATAATCAATTAGCAGCTTATGTGGTTTCTAGTTTTCGGGTA 1200
 381 Q M T R R W D N Q L A A Y V V S S F R V 400
 1201 GCTAAGTTGGCAATGGTTGGGAGCAAGGAGTACAACCTCATTCAAAGATGGTTATTGTG 1260
 401 A K L A M V G Q Q G V Q L I Q K M V I V 420
 1261 GCAACTCTATGGATTGGTGCAAAATTGGTAATTGAAGGCAAGCTATCGGTAGGTCAATTA 1320
 421 A T L W I G A K L V I E G K L S V G Q L 440

mxb
 mxb 13

FIG 8-1

1321	ATAGCATTTAATATGCTGGCAGGTGAGTGGCCGCTCTGTTATCCGCCTGGCACAGCTA	1380
441	I A F N M L A G Q V A A P V I R' L A' Q L	460
1381	TGGCAAGATTTTCAGCAAGTAGGTATTTAGTGGCGAGATTGGGTGATATTTAAATACT	1440
461	W Q D F Q Q V G I S V A R L G D I L N T	480
1441	CCAAGTGGCATTCTACATCTCGCTTAACCTTACCTGATATTAAGGGTGATATTACATTT	1500
481	P T E H S T S R L T L P D I K G D I T F	500
1501	GAAATGTTGATTTTCGCTACAAAATAGATGGGCATTTAATATTACAGAATTTAAATTTA	1560
501	E N V D F R Y K I D G H L I L Q N L N L	520
1561	CAGATTAACGCTGGAGAGATACTAGGTATCGTAGGACGCTCTGGTTCAGGTAAATCAACA	1620
521	Q I N A G E I L G I V G R S G S G K S T	540
1621	TTGACAAAATTAGTACAGCGTTTATATGTACCAGAAAATGGGCGAATATTAGTTGATGGA	1680
541	L T K L V Q R L Y V P E N G R I L V D G	560
1681	AACGATTTGGCATTAGCTGATCCCGCTTGGCTGCGTCGCCAAGTGGGTGTTGTTTTGCAG	1740
561	N D L A L A D P A W L R R Q V G V V L Q	580
1741	GAAATGTGTTACTCAATCGTAGTATTCGAGATAATATTGCCCTAACTGATACGGGCATG	1800
581	E N V L L N R S I R D N I A L T D T G M	600
1801	TCATTAGAGTTTATTATCCAGGCTGCCAAGATGTCTGGGGCACATGACTTTATTATGGAA	1860
601	S L E F I I Q A A K M S G A H D F I M E	620
1861	TTGCCTGAGGGTTATGATACGATTGTTGGAGAGCAAGGTGCAGGCTTGTGAGGTGGACAA	1920
621	L P E G Y D T I V G E Q G A G L S G G Q	640
1921	CGCCAGCGTATCGCTATTGCGCGTGCTTTAATTACCAATCCGCGTATTTTGATTTTGTAT	1980
641	R Q R I A I A R A L I T N P R I L I F D	660
1981	GAAGCTACTAGTGCATTAGACTATGAGTCGGAAAGGGCTATTATGCAAAATATGCAGGCA	2040
661	E A T S A L D Y E S E R A I M Q N M Q A	680
2041	ATTTGCCAAGGTAGAACAGTGTGATTATTGCACATCGCTTATCTACCGTAAAAATGGCA	2100
681	I C Q G R T V L I I A H R L S T V K M A	700
2101	CATCGCATTATTGCAATGGACAAGGGGAAAATTGTAGAGCAAGGCACACATCAAGAATTG	2160
701	H R I I A M D K G K I V E Q G T H Q E L	720
2161	TTGCAAAAAGAAGATGGTTACTATCGTTATTTATATGATTTGCAGAATGGATAAA	2215
721	L Q K E D G Y Y R Y L Y D L Q N G *	739

F168-2

SEQ ID NO: 30
SEQ ID NO: 18

F15.9

Mbx8	- - - - - MFD	XAQQPAPSA	TUULAKY G	TSASPA IM	HQFSNTRG	DNEISN L	AAKKLEL	55
Lkt8	M - A W Q RND	L GVA	LTMLAQEN	PSLSPERL	EFDDDGAG	ISGAMLL	AAKSLAP	56
ApX18	MDFYRE . FD	L GVA	LTMLAQEN	IAVFEER	KKVLL GRG	LUKTAVLL	AAKSLAP	55
Hly8	MDSC K . FD	L GVA	LTMLAQEN	SVRFEER	LPDTGGTG	LGKTSWLL	AAKSLAP	55
Mbx8	VVI I I N O P	RLSMHTT F	ALVWCONKP	DLDQNLNS	FILTRIDGV	GSAAKVLIV	DLI NRP	116
Lkt8	AAKHIIKKKAT	SRRLNLL	ALVWQDN GKE	FILTRIDGV	T NNRKLLI	NLQDAP	107
ApX18	AAKHIIKKKAT	SRRLNLL	ALVWQDN GKE	FILTRIDGV	NRAKKLLI	DLI NRP	106
Hly8	AAKHIIKKKAT	SRRLNLL	ALVWQDN GKE	FILTRIDGV	KEANRLLI	DLI NRP	106
Mbx8	ILLAGEFS	RRYSCKLML	VTGRASILG	SLAKPFTW	PIPAVIRIR	YIFFEVIV	SVVLQIF	177
Lkt8	QILSTDESE	ACIRGQILIL	VISRASVVG	QLAKPFTW	PIPAVIRIR	KIP SRLIV	SVVLQIF	168
ApX18	RIISQARSE	SKIRGRLIL	VASRASVVG	KLAKPFTW	PIPAVIRIR	KIP SRLIV	SVVLQIF	167
Hly8	NLEQSESE	ALYQGH IL	ASRSVAG	KLAKPFTW	PIPAVIRIR	YIFIRLV	SVVLQIF	167
Mbx8	ALITPLFPQ	VUMDXVLVH	RCPSTLUV	AALLVVS	FEILSGLR	TYIPARST	RIDVRLG	238
Lkt8	ALITPLFPQ	VUMDXVLVH	RCPSTLUV	TVALAIV	FEIVLSGLR	TYIPARST	RIDVRLG	229
ApX18	ALITPLFPQ	VUMDXVLVH	RCPSTLUV	TVALAIV	FEIVLSGLR	TYIPARST	RIDVRLG	228
Hly8	ALITPLFPQ	VUMDXVLVH	RCPSTLUV	TVALAIV	FEIVLSGLR	TYIPARST	RIDVRLG	228
Mbx8	ARLPRELLA	LPATFESR	RVGDTVAR	RHLHILMF	LTGQALTSV	LDLVFSPFV	LPVNNY	299
Lkt8	AKLPRELLS	LPISIFENR	RVGDTVAR	RELDQIRNF	LTGQALTSV	LDLVFSPFV	PAVNNY	290
ApX18	AKLPRELLS	LPISIFENR	RVGDTVAR	RELDQIRNF	LTGQALTSV	LDLVFSPFV	PAVNNY	289
Hly8	AKLPRELLS	LPISIFENR	RVGDTVAR	RELDQIRNF	LTGQALTSV	LDLVFSPFV	PAVNNY	289
Mbx8	SPRLTLVIL	ASLPIYAFW	SAFISPILE	TLNDQFAR	NADNQSFV	ESVTAIGT	KAAVCE	360
Lkt8	SPRLTLVIL	GSPLCYILW	SIFISPILE	RELDKPAR	SADNQAFV	ESVTAIGT	KAAVCE	351
ApX18	SPRLTLVIL	GSPLCYILW	SIFISPILE	RELDKPAR	SADNQAFV	ESVTAIGT	KAAVCE	350
Hly8	SPRLTLVIL	GSPLCYILW	SIFISPILE	RELDKPAR	SADNQAFV	ESVTAIGT	KAAVCE	350
Mbx8	QMTTRWDNQ	LAAVVS SF	RVAKLAMG	QQCVLIQ	MVIVATLW	GAKLVIEGK	LSGQLI	421
Lkt8	QMTTRWDNQ	LAAVVS SF	RVAKLAMG	QQCVLIQ	MVIVATLW	GAKLVIEGK	LSGQLI	412
ApX18	QMTTRWDNQ	LAAVVS SF	RVAKLAMG	QQCVLIQ	MVIVATLW	GAKLVIEGK	LSGQLI	411
Hly8	QMTTRWDNQ	LAAVVS SF	RVAKLAMG	QQCVLIQ	MVIVATLW	GAKLVIEGK	LSGQLI	411
Mbx8	AFNMLAGQV	AAPVIRLQ	LWQDPQVVG	ISVARLGD	LNTPTESK	S LTLPLIK	GDITPRN	482
Lkt8	AFNMLAGQV	AAPVIRLQ	LWQDPQVVG	ISVARLGD	LNTPTESK	S LTLPLIK	GDITPRN	473
ApX18	AFNMLAGQV	AAPVIRLQ	LWQDPQVVG	ISVARLGD	LNTPTESK	S LTLPLIK	GDITPRN	472
Hly8	AFNMLAGQV	AAPVIRLQ	LWQDPQVVG	ISVARLGD	LNTPTESK	S LTLPLIK	GDITPRN	472
Mbx8	IRPRIKIDG	HLILOMLNL	QINAGSGG	IVGRSGSG	STLTNLQR	LYFENGRT	LIDGNDL	543
Lkt8	IRPRIKIDG	HLILOMLNL	QINAGSGG	IVGRSGSG	STLTNLQR	LYFENGRT	LIDGNDL	534
ApX18	IRPRIKIDG	HLILOMLNL	QINAGSGG	IVGRSGSG	STLTNLQR	LYFENGRT	LIDGNDL	533
Hly8	IRPRIKIDG	HLILOMLNL	QINAGSGG	IVGRSGSG	STLTNLQR	LYFENGRT	LIDGNDL	533
Mbx8	ALADPAWLR	ROVGVVLQ	NVLLNRSIR	DNIALDIFG	MSSEFIQA	AKMSGARDP	IMELPEG	604
Lkt8	ALADPAWLR	ROVGVVLQ	NVLLNRSIR	DNIALDIFG	MSSEFIQA	AKMSGARDP	IMELPEG	595
ApX18	ALADPAWLR	ROVGVVLQ	NVLLNRSIR	DNIALDIFG	MSSEFIQA	AKMSGARDP	IMELPEG	594
Hly8	ALADPAWLR	ROVGVVLQ	NVLLNRSIR	DNIALDIFG	MSSEFIQA	AKMSGARDP	IMELPEG	594
Mbx8	YDTIVGEQG	AGLSGGQR	RIAIARALV	TNPILIFD	EATSALDYE	SERAIMQNM	QAICQGR	665
Lkt8	YDTIVGEQG	AGLSGGQR	RIAIARALV	TNPILIFD	EATSALDYE	SERAIMQNM	QAICQGR	656
ApX18	YDTIVGEQG	AGLSGGQR	RIAIARALV	TNPILIFD	EATSALDYE	SERAIMQNM	QAICQGR	655
Hly8	YDTIVGEQG	AGLSGGQR	RIAIARALV	TNPILIFD	EATSALDYE	SERAIMQNM	QAICQGR	655
Mbx8	TVIIIAHRL	STVKNADRI	IAMRGKIV	EQGKHELL	QKEDGYTF	LYDLQNG	717	
Lkt8	TVIIIAHRL	STVKNADRI	IAMRGKIV	EQGKHELL	QKEDGYTF	LYDLQNG	708	
ApX18	TVIIIAHRL	STVKNADRI	IAMRGKIV	EQGKHELL	QKEDGYTF	LYDLQNG	707	
Hly8	TVIIIAHRL	STVKNADRI	IAMRGKIV	EQGKHELL	QKEDGYTF	LYDLQNG	707	

SERIDNO: 18
SERIDNO: 19
SERIDNO: 20
SERIDNO: 21

FIG. 10

DNASIS Translation Editor [11-00 C gene.dna]

1	ATGACGAAAAAGTTTGCAGAGCTAGGTTTAATTGCATGGCTTTGGTCTAACTCTGATATG	60
1	M T K K F A E L G L I A W L W S N S D M	20
61	CATAAACATTGGACGTTGTCTTTGTTTGGACCAATGTTATCCGGCAATTGAGACAGGT	120
21	H K H W T L S L F A T N V I P A I E T G	40
121	CAATATGTTATATTGAAAAGAGAAGATATGCCTGTAGCATATTGTAGTTGGGCTAACTT	180
41	Q Y V I L K R E D M P V A Y C S W A K L	60
181	AGTTTAGAAAACGAGGTTAAATATATTAACGATGTTACTTCTCTTAAGTTAGATGACTGG	240
61	S L E N E V K Y I N D V T S L K L D D W	80
241	CAGTCAGGTGACCGAAACTGGTTTATTGACTGGATTGCTCCATTTGGCGATAGTCTTACA	300
81	Q S G D R N W F I D W I A P F G D S L T	100
301	CTCACAAAACACATGAGAACGTTATTTTCAGATGAATTGTTTAGAGCGATTCTGTAGAT	360
101	L T K H M R T L F S D E L F R A I R V D	120
361	GGAAATTCATCGCATGGTAAGATATCTGAATTTTATGGAAAGTCTGTTGATTCAAAATTA	420
121	G N S S H G K I S E F Y G K S V D S K L	140
421	GCCTCAAGAATATTTGCACAATATCACGAAGATTTGACGAGCAAATTGTCAACTCAGAAT	480
141	A S R I F A Q Y H E D L T S K L S T Q N	160
481	AATTTTATTATATCTAAAGATAATTA	507
161	N F I I S K D N *	169

SEQ ID NO: 31
SEQ ID NO: 32

mbx C
Mbx C

[illegible]

MbxC	G	K	S	V	D	S	K	L	A	S	I	F	A	Q	Y	H	E	L	T	S	K	L	S	T	Q	N	N	F	I	S	K	D	N	-	168					
LktC	K	G	G	K	I	D	D	K	T	A	K	K	R	F	D	T	Y	Q	E	E	L	A	T	A	S	E	L	K	N	E	F	N	F	I	K	K	-	-	-	167
ApxIC	H	G	G	K	I	D	K	K	L	A	S	K	I	F	Q	Y	H	F	E	L	M	S	E	L	K	N	K	Q	N	F	K	F	S	L	V	N	S	172		
HlyC	H	G	G	K	I	D	K	Q	L	A	N	K	I	F	K	Q	Y	H	F	E	L	L	I	T	E	V	K	N	K	S	D	F	N	F	S	L	T	G	-	170

SEQ 1D NO : 2
SEQ 1D NO : 3
SEQ 1D NO : 5
SEQ 1D NO : 7

1321 CCAGGAATGAATGTTACTGCTGAAATTAACAGGTAAACGTCGTGTTTGGATTATATA 1380
441 P G M N V T A E I K T G K R R V L D Y I 460

1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R * 476

SEQ ID NO: 36 }
SEQ ID NO 37 }

FIG. 12-2

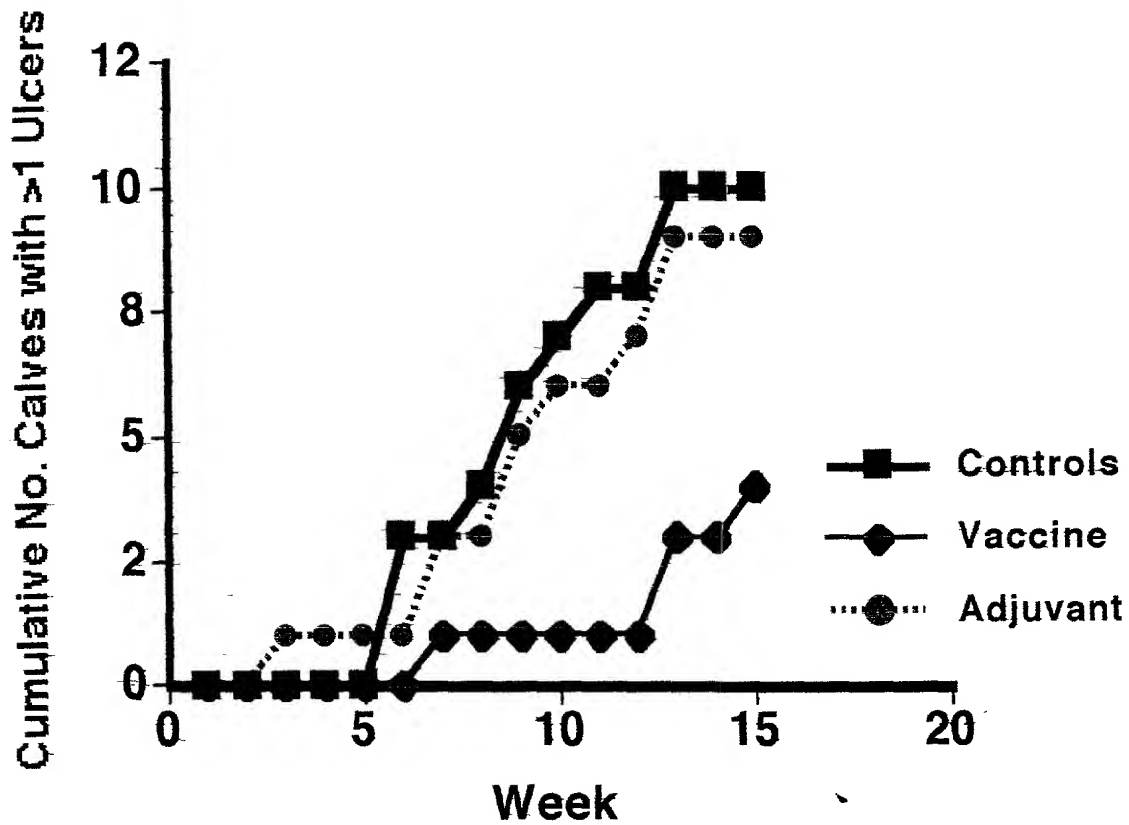
1321 CCAGGAATGAATGTTACTGCTGAAATTAACAGGTAAACGTCGTGTTTGGATTATATA 1380
441 P G M N V T A E I K T G K R R V L D Y I 460
1381 TTAAGTCCATTGCAGACAAAAGTTGATGAAAGTTTTCGAGAACGCTAA 1428
461 L S P L Q T K V D E S F R E R * 476

FIG. 13

MbxD	--MF--QA LK	FF RYITVWR	NTWA RDOLT	PPKRTK ELA	FLPAHLELT	48
LktD	MKIWLSG YE	PFLRYRN WA	EVWKIRK LD	HPNKRDESE	FLPAHLELIE	50
ApxD	MKTWLMGLYE	PFORIKTVWT	ELWKIRHOLD	TPDREKDENE	FLPAHLELIE	50
HlyD	MKTWLMGFS E	ELRYKLVWS	ETWRIRKOLD	TPVREKDENE	FLPAHLELIE	50
MbxD	TPVS RSS WT	AR IM FVLF	ALLNSWVGQ	IVATASGR	SSGSRSKTIQ	98
LktD	TPVS KKRPLI	AYLIMLFLVV	AVLASVSKV	EIVATAPGRL	TFSGRSKEIK	100
ApxD	TPVS KKRPLI	AYLIMLFLFL	ALV SIVSHV	EIVATATGRL	AFSDRSKEIK	100
HlyD	TPVS R PRLL	AYFIMGFEVI	AF LSVLGQV	EIVATANGRK	TLSGRSKEIK	100
MbxD	S ETATVKA	V DGNV Q	G LVDLVG	GS DSDVAQSE	KALRAAQLSK	148
LktD	PIENAIVQEI	PVKDGGFVER	GQLLVSLTAL	GS DADI KKT M	ASLSLAKLEN	150
ApxD	PIENA VKEI	PVQDGGFVER	DQLLHLTAL	GADADQ QRTK	SSLSLTKLER	150
HlyD	PIENSIVKEI	IVK G SVRK	GDVLLKLTAL	GA ADTLKTQ	SSL LQA LEQ	150
MbxD	LRL EA LSA	NHRINEQIDV	AYAKSL MIS	ESEINEAQT	AQNOYQAWLA	197
LktD	YRYQTLLTAT	EKESLBIIDL	.SRTEFRDSS	EEDRLRIKHL	IERQYTTWQN	199
ApxD	YRYE LLEA	AADRLPLI L	.TKDEFN HAT	EEDKTRI RYL	ITEQF EAWQN	199
HlyD	IRYQTLRSR	ELNKLPE KL	PDEPYFQNV	EEV LR TS	IKEQF STWQN	200
MbxD	QDEQLKLTLR	GHTAELQ SAR	SQEQLVSVG	AI EH KTD	RSLKAENFIS	247
LktD	QKTQKTLAYR	RKEABKQ TIF	AY RKYEG	RIEQEKLKDF	KALYKQKS S	249
ApxD	QKYQKELALQ	R EAKQT L	ANIRKYEG S	RVENERL KDL	KKLFNSKSTS	249
HlyD	QKYQKELNLD	KRAE L TIL	ARIN YENVS	RVEKSRLDDF	RSL LHKQATA	250
MbxD	EHAYLEQESR	L SNQNLQS	TRSQ OKINA	AI QAE NRM	LYTONLKRDT	297
LktD	KHEL LAQENK	LIEAQMVA V	YRSKLNE EN	DL LN VKEELE	LITQFFKSD	299
ApxD	KHDVLTQEE	HIEAVMEI AV	YKSRLNE ES	DL RQAKEEIH	LITQF ADI	299
HlyD	KBAVLEQENK	Y EAANELRV	YKSOLEIES	LSAKEEYQ	L TOLPKNI	300
MbxD	LES LROTNEQ	INQYTG TNR	AKORQKLLSI	SPVNGTQ	LTA TLGGVV	347
LktD	LEKLKOHIE N	EROLRLLELEK	NNORRQASMI	RAPVSGTVQQ	LKIHTIGGVV	349
ApxD	LEKLKONVEA	EKQLSLLELEK	NEORQHASVI	RAPVSGTVQQ	LKTHTVGGVV	349
HlyD	LEKLROTTS	IELLTLELEK	NE RQQASVI	RAPVSGRVQQ	LKVHTEGGVV	350
MbxD	QAATK MVTA	PNDNQVEVEV	LVLNKDIGFV	KAGONVLIK	ESFPYTRYGY	397
LktD	TTAETLM IV	PEDDVLEATA	LVPNKDIGFV	AAGQEVIIKV	ETFPYTRYGY	399
ApxD	TTAETLMVIA	PEDDVLEVTA	L QNKDIGFI	EVGQDAIKV	ETFPYTRYGY	399
HlyD	TTAETLMVIV	PEDDTLEVTA	LVQNKDIGFI	NV GQNAIIKV	EAFPYTRYGY	400
MbxD	LTGRIKSI SH	DAIEHQHLGL	VNTAVS ED	STIN IDGVT	INLT PGMNVT	446
LktD	LTGRIKHISP	DAIEQPNVGL	VFNATIAIDR	KNLTSPDGK	IDLSSGMTT	449
ApxD	LMGKVRNITL	AIENPQLGL	VPNSTISIDR	KTLSGKDGKE	IELGSGMSVT	449
HlyD	LVGKVRNINL	DAIEDQKLGL	VPNVIVS E	NDLST GNRH	IFLSSGMAVT	449
MbxD	ARIKTGKR RV	MDYLSPLT	KVDESFRER	475	SED ID NO: 37	
LktD	ARIKTGERSV	MSYLLSPLLE	SVTESLRER	478	SEQ ID NO: 38	
ApxD	ARIKTGERSV	ISYLLSPLLE	SVSES LRER	478	SEQ ID NO: 39	
HlyD	ARIKTGMRSV	ISYLLSPLLE	SVTESLHER	478	SEA ID NO: 40	

F16.14

Cumulative Number of Calves With Severe Ulcers



Number of calves with ulcers with clinical scores >+2

F1615

Number of calves affected each week

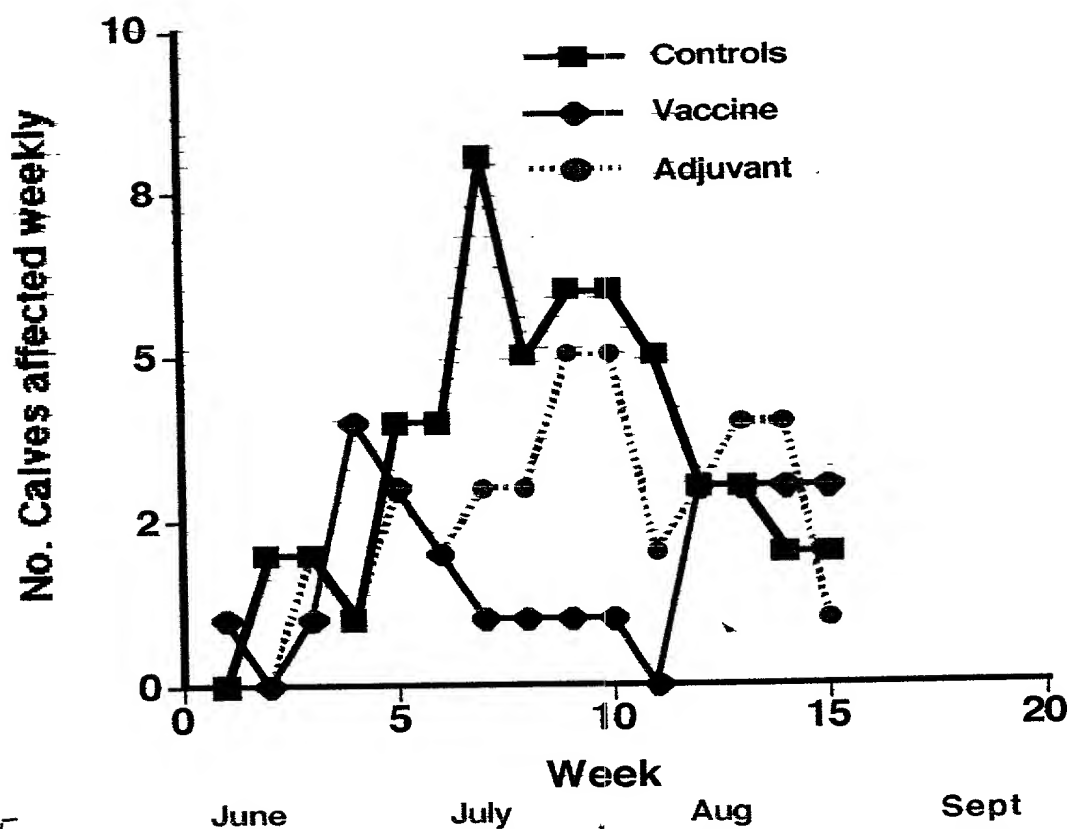
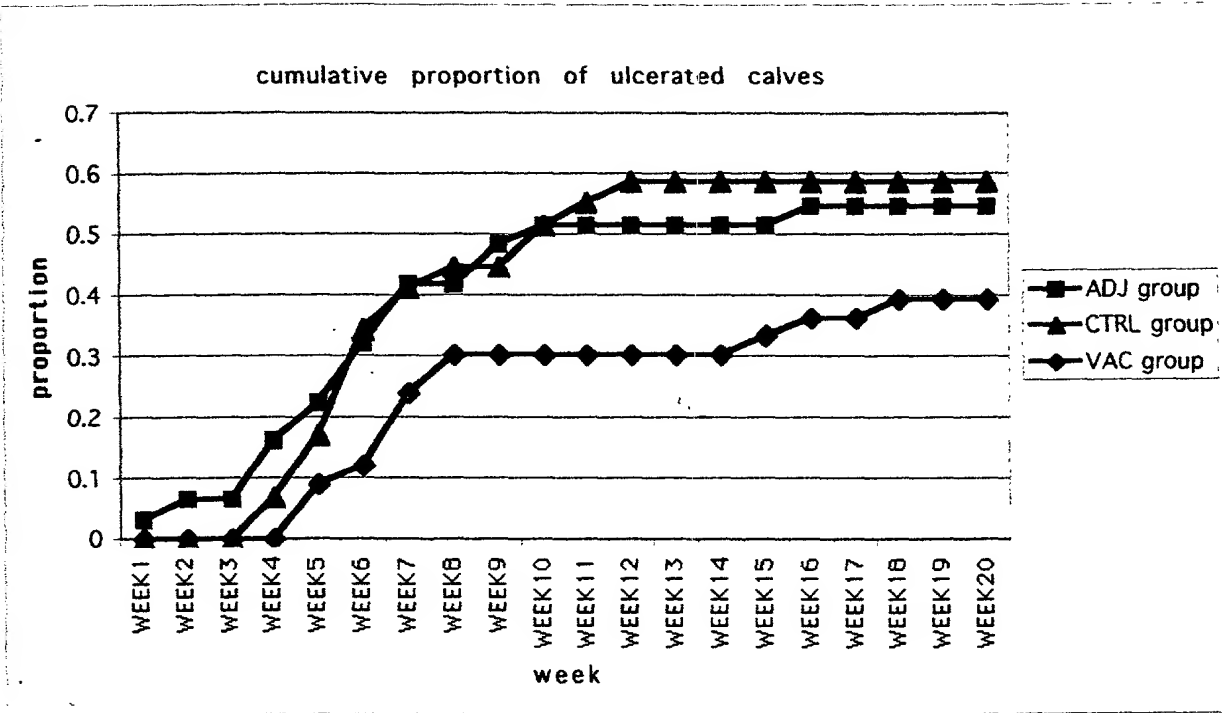


Figure 15
Number of calves affected weekly in 1 group of vaccinated calves and in controls.

FIG. 16



Cumulative proportion of ulcerated calves during the trial. Calves received as vaccines either saline (designated 'CTRL'), adjuvant alone (designated 'ADJ'), or the recombinant cytotoxin vaccine (designated 'VAC').